

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gerard, Craig
Gerard, Norma P.
Mackay, Charles
Ponath, Paul D.
Post, Theodore W.
Qin, Shixin

(ii) TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
ANTAGONISTS THEREOF

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
(B) STREET: Two Militia Drive
(C) CITY: Lexington
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02173

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/375,199
(B) FILING DATE: 19-JAN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brook, David E.
(B) REGISTRATION NUMBER: 22,592
(C) REFERENCE/DOCKET NUMBER: LKS94-05A PCT

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

1689 3636 5283 6930 8577 10224 11871 13518 15165 16812 18459 20106 21753 23400 25047 26694 28341 29988 31635 33282 34929 36576 38223 39870 41517 43164 44811 46458 48105 49752 51399 53046 54693 56340 57987 59634 61281 62928 64575 66222 67869 69516 71163 72810 74457 76104 77751 79398 81045 82692 84339 85986 87633 89280 90927 92574 94221 95868 97515 99162 100809 102456 104103 105750 107397 109044 110691 112338 113985 115632 117279 118926 120573 122220 123867 125514 127161 128808 130455 132102 133749 135396 137043 138690 140337 141984 143631 145278 146925 148572 150219 151866 153513 155160 156807 158454 160101 161748 163395 165042 166689 168336 169983 171630 173277 174924 176571 178218 179865 181512 183159 184806 186453 188100 189747 191394 193041 194688 196335 197982 199629 201276 202923 204570 206217 207864 209511 211158 212805 214452 216099 217746 219393 221040 222687 224334 225981 227628 229275 230922 232569 234216 235863 237510 239157 240804 242451 244098 245745 247392 249039 250686 252333 253980 255627 257274 258921 260568 262215 263862 265509 267156 268803 270450 272097 273744 275391 277038 278685 280332 281979 283626 285273 286920 288567 290214 291861 293508 295155 296802 298449 300096 301743 303390 305037 306684 308331 309978 311625 313272 314919 316566 318213 319860 321507 323154 324801 326448 328095 329742 331389 333036 334683 336330 337977 339624 341271 342918 344565 346212 347859 349506 351153 352800 354447 356094 357741 359388 361035 362682 364329 365976 367623 369270 370917 372564 374211 375858 377505 379152 380799 382446 384093 385740 387387 389034 390681 392328 393975 395622 397269 398916 400563 402210 403857 405504 407151 408798 410445 412092 413739 415386 417033 418680 420327 421974 423621 425268 426915 428562 430209 431856 433503 435150 436797 438444 440091 441738 443385 445032 446679 448326 449973 451620 453267 454914 456561 458208 459855 461502 463149 464796 466443 468090 469737 471384 473031 474678 476325 477972 479619 481266 482913 484560 486207 487854 489501 491148 492795 494442 496089 497736 499383 501030 502677 504324 505971 507618 509265 510912 512559 514206 515853 517500 519147 520794 522441 524088 525735 527382 529029 530676 532323 533970 535617 537264 538911 540558 542205 543852 545499 547146 548793 550440 552087 553734 555381 557028 558675 560322 561969 563616 565263 566910 568557 570204 571851 573498 575145 576792 578439 580086 581733 583380 585027 586674 588321 589968 591615 593262 594909 596556 598203 599850 601497 603144 604791 606438 608085 609732 611379 613026 614673 616320 617967 619614 621261 622908 624555 626202 627849 629496 631143 632790 634437 636084 637731 639378 641025 642672 644319 645966 647613 649260 650907 652554 654201 655848 657495 659142 660789 662436 664083 665730 667377 669024 670671 672318 673965 675612 677259 678906 680553 682200 683847 685494 687141 688788 690435 692082 693729 695376 697023 698670 700317 701964 703611 705258 706905 708552 710199 711846 713493 715140 716787 718434 720081 721728 723375 725022 726669 728316 729963 731610 733257 734904 736551 738198 739845 741492 743139 744786 746433 748080 749727 751374 753021 754668 756315 757962 759609 761256 762903 764550 766197 767844 769491 771138 772785 774432 776079 777726 779373 781020 782667 784314 785961 787608 789255 790902 792549 794196 795843 797490 799137 800784 802431 804078 805725 807372 809019 810666 812313 813960 815607 817254 818901 820548 822195 823842 825489 827136 828783 830430 832077 833724 835371 837018 838665 840312 841959 843606 845253 846900 848547 850194 851841 853488 855135 856782 858429 860076 861723 863370 865017 866664 868311 869958 871605 873252 874899 876546 878193 879840 881487 883134 884781 886428 888075 889722 891369 893016 894663 896310 897957 899604 901251 902898 904545 906192 907839 909486 911133 912780 914427 916074 917721 919368 921015 922662 924309 925956 927603 929250 930897 932544 934191 935838 937485 939132 940779 942426 944073 945720 947367 949014 950661 952308 953955 955602 957249 958896 960543 962190 963837 965484 967131 968778 970425 972072 973719 975366 977013 978660 980307 981954 983601 985248 986895 988542 990189 991836 993483 995130 996777 998424 1000071 1001718 1003365 1005012 1006659 1008306 1009953 1011600 1013247 1014894 1016541 1018188 1019835 1021482 1023129 1024776 1026423 1028070 1029717 1031364 1033011 1034658 1036305 1037952 1039599 1041246 1042893 1044540 1046187 1047834 1049481 1051128 1052775 1054422 1056069 1057716 1059363 1061010 1062657 1064304 1065951 1067598 1069245 1070892 1072539 1074186 1075833 1077480 1079127 1080774 1082421 1084068 1085715 1087362 1089009 1090656 1092303 1093950 1095597 1097244 1098891 1100538 1102185 1103832 1105479 1107126 1108773 1110420 1112067 1113714 1115361 1117008 1118655 1120302 1121949 1123596 1125243 1126890 1128537 1130184 1131831 1133478 1135125 1136772 1138419 1140066 1141713 1143360 1145007 1146654 1148301 1149948 1151595 1153242 1154889 1156536 1158183 1159830 1161477 1163124 1164771 1166418 1168065 1169712 1171359 1173006 1174653 1176300 1177947 1179594 1181241 1182888 1184535 1186182 1187829 1189476 1191123 1192770 1194417 1196064 1197711 1199358 1201005 1202652 1204299 1205946 1207593 1209240 1210887 1212534 1214181 1215828 1217475 1219122 1220769 1222416 1224063 1225710 1227357 1229004 1230651 1232298 1233945 1235592 1237239 1238886 1240533 1242180 1243827 1245474 1247121 1248768 1250415 1252062 1253709 1255356 1257003 1258650 1260297 1261944 1263591 1265238 1266885 1268532 1270179 1271826 1273473 1275120 1276767 1278414 1280061 1281708 1283355 1285002 1286649 1288296 1289943 1291590 1293237 1294884 1296531 1298178 1300825 1302472 1304119 1305766 1307413 1309060 1310707 1312354 1314001 1315648 1317295 1318942 1320589 1322236 1323883 1325530 1327177 1328824 1330471 1332118 1333765 1335412 1337059 1338706 1340353 1342000 1343647 1345294 1346941 1348588 1350235 1351882 1353529 1355176 1356823 1358470 1360117 1361764 1363411 1365058 1366705 1368352 1369999 1371646 1373293 1374940 1376587 1378234 1379881 1381528 1383175 1384822 1386469 1388116 1389763 1391410 1393057 1394704 1396351 1397998 1399645 1401292 1402939 1404586 1406233 1407880 1409527 1411174 1412821 1414468 1416115 1417762 1419409 1421056 1422703 1424350 1425997 1427644 1429291 1430938 1432585 1434232 1435879 1437526 1439173 1440820 1442467 1444114 1445761 1447408 1449055 1450702 1452349 1453996 1455643 1457290 1458937 1460584 1462231 1463878 1465525 1467172 1468819 1470466 1472113 1473760 1475407 1477054 1478701 1480348 1481995 1483642 1485289 1486936 1488583 1490230 1491877 1493524 1495171 1496818 1498465 1500112 1501759 1503406 1505053 1506700 1508347 1509994 1511641 1513288 1514935 1516582 1518229 1519876 1521523 1523170 1524817 1526464 1528111 1529758 1531405 1533052 1534699 1536346 1537993 1539640 1541287 1542934 1544581 1546228 1547875 1549522 1551169 1552816 1554463 1556110 1557757 1559404 1561051 1562698 1564345 1565992 1567639 1569286 1570933 1572580 1574227 1575874 1577521 1579168 1580815 1582462 1584109 1585756 1587403 1589050 1590697 1592344 1593991 1595638 1597285 1598932 1600579 1602226 1603873 1605520 1607167 1608814 1610461 1612108 1613755 1615402 1617049 1618696 1620343 1621990 1623637 1625284 1626931 1628578 1630225 1631872 1633519 1635166 1636813 1638460 1640107 1641754 1643401 1645048 1646695 1648342 1649989 1651636 1653283 1654930 1656577 1658224 1659871 1661518 1663165 1664812 1666459 1668106 1669753 1671400 1673047 1674694 1676341 1677988 1679635 1681282 1682929 1684576 1686223 1687870 1689517 1691164 1692811 1694458 1696105 1697752 1699399 1701046 1702693 1704340 1705987 1707634 1709281 1710928 1712575 1714222 1715869 1717516 1719163 1720810 1722457 1724104 1725751 1727398 1729045 1730692 1732339 1733986 1735633 1737280 1738927 1740574 1742221 1743868 1745515 1747162 1748809 1750456 1752103 1753750 1755397 1757044 1758691 1760338 1761985 1763632 1765279 1766926 1768573 1770220 1771867 1773514 1775161 1776808 1778455 1780102 1781749 1783396 1785043 1786690 1788337 1789984 1791631 1793278 1794925 1796572 1798219 1800866 1802513 1804160 1805807 1807454 1809101 1810748 1812395 1814042 1815689 1817336 1818983 1820630 1822277 1823924 1825571 1827218 1828865 1830512 1832159 1833806 1835453 1837100 1838747 1840394 1842041 1843688 1845335 1846982 1848629 1850276 1851923 1853570 1855217 1856864 1858511 1860158 1861805 1863452 1865099 1866746 1868393 1870040 1871687 1873334 1874981 1876628 1878275 1879922 1881569 1883216 1884863 1886510 1888157 1889804 1891451 1893098 1894745 1896392 1898039 1900686 1902333 1903980 1905627 1907274 1908921 1910568 1912215 1913862 1915509 1917156 1918803 1920450 1922097 1923744 1925391 1927038 1928685 1930332 1931979 1933626 1935273 1936920 1938567 1940214 1941861 1943508 1945155 1946802 1948449 1950096 1951743 1953390 1955037 1956684 1958331 1959978 1961625 1963272 1964919 1966566 1968213 1969860 1971507 1973154 1974801 1976448 1978095 1979742 1981389 1983036 1984683 1986330 1987977 1989624 1991271 1992918 1994565 1996212 1997859 1999506 2001153 2002800 2004447 2006094 2007741 2009388 2011035 2012682 2014329 2015976 2017623 2019270 2020917 2022564 2024211 2025858 2027505 2029152 2030799 2032446 2034093 2035740 2037387 2039034 2040681 2042328 2043975 2045622 2047269 2048916 2050563 2052210 2053857 2055504 2057151 2058798 2060445 2062092 2063739 2065386 2067033 2068680 2070327 2071974 2073621 2075268 2076915 2078562 2080209 2081856 2083503 2085150 2086797 2088444 2090091 2091738 2093385 2095032 2096679 2098326 2100600 2102250 2103900 2105550 2107200 2108850 2110500 2112150 2113800 2115450 2117100 2118750 2120400 2122050 2123700 2125350 2127000 2128650 2130300 2131950 2133600 2135250 2136900 2138550 2140200 2141850 2143500 2145150 2146800 2148450 2150100 2151750 2153400 2155050 2156700 2158350 2160000 2161650 2163300 2164950 2166600 2168250 2169900 2171550 2173200 2174850 2176500 2178150 2179800 2181450 2183100 2184750 2186400 2188050 2189700 2191350 2193000 2194650 2196300 2197950 2199600 2201250 2202900 2204550 2206200 2207850 2209500 2211150 2212800 2214450 2216100 2217750 2219400 2221050 2222700 2224350 2226000 2227650 2229300 2230950 2232600 2234250 2235900 2237550 2239200 2240850 2242500 2244150 2245800 2247450 2249100 2250750 2252400 2254050 2255700 2257350 2259000 2260650 2262300 2263950 2265600 2267250 2268900 2270550 2272200 2273850 2275500 2277150 2278800 2280450 2282100 2283750 2285400 2287050 2288700 2290350 2292000 2293650 2295300 2296950 2298600 2300250 2301900 2303550 2305200 2306850 2308500 2310150 2311800 2313450 2315100 2316750 2318400 2320050 2321700 2323350 2325000 2326650 2328300 2329950 2331600 2333250 2334900 2336550 2338200 2339850 2341500 2343150 2344800 2346450 2348100 2349750 2351400 2353050 2354700 2356350 2358000 2359650 2361300 2362950 2364600 2366250 2367900 2369550 2371200 2372850 2374500 2376150 2377800 2379450 2381100 2382750 2384400 2386050 2387700 2389350 2391000 2392650 2394300 2395950 2397600 2399250 2400900 2402550 2404200 2405850 2407500 2409150 2410800 2412450 2414100 2415750 2417400 2419050 2420700 2422350 2424000 2425650 2427300 2428950 2430600 2432250 2433900 24355

AATCCTTTTC	CTGGCACCTC	TGATATCCTT	TTGAAATTCA	TGTTAAAGAA	TCCCTAGGCT	60
GCTATCACAT	GTGGCATCTT	TGTTGAGTAC	ATGAATAAAT	CAACTGGTGT	GTTTTACGAA	120
GGATGATTAT	GCTTCATTGT	GGGATTGTAT	TTTTCTTCTT	CTATCACAGG	GAGAAGTGAA	180
ATGACAACCT	CACTAGATAC	AGTTGAGACC	TTTGGTACCA	CATCCTACTA	TGATGACGTG	240
GGCCTGCTCT	GTGAAAAAGC	TGATACCAGA	GCACTGATGG	CCCAGTTTGT	GCCCCCGCTG	300
TACTCCCTGG	TGTTCACTGT	GGGCCTCTTG	GGCAATGTGG	TGGTGGTGAT	GATCCTCATA	360
AAATACAGGA	GGCTCCGAAT	TATGACCAAC	ATCTACCTGC	TCAACCTGGC	CATTTCCGAC	420
CTGCTCTTCC	TCGTCACCCT	TCCATTCTGG	ATCCACTATG	TCAGGGGGCA	TAActGGGTT	480
TTTGGCCATG	GCATGTGTAA	GCTCCTCTCA	GGGTTTTATC	ACACAGGCTT	GTACAGCGAG	540
ATCTTTTTTCA	TAATCCTGCT	GACAATCGAC	AGGTACCTGG	CCATTGTCCA	TGCTGTGTTT	600
GCCCTTCGAG	CCCGGACTGT	CACTTTTGGT	GTCATCACCA	GCATCGTCAC	CTGGGGCCTG	660
GCAGTGCTAG	CAGCTCTTCC	TGAATTTATC	TTCTATGAGA	CTGAAGAGTT	GTTTGAAGAG	720
ACTCTTTGCA	GTGCTCTTTA	CCCAGAGGAT	ACAGTATATA	GCTGGAGGCA	TTTCCACACT	780
CTGAGAATGA	CCATCTTCTG	TCTCGTTCTC	CCTCTGCTCG	TTATGGCCAT	CTGCTACACA	840
GGAATCATCA	AAACGCTGCT	GAGGTGCCCC	AGTAAAAAAA	AGTACAAGGC	CATCCGGCTC	900
ATTTTTGTCA	TCATGGCGGT	GTTTTTTCATT	TTCTGGACAC	CCTACAATGT	GGCTATCCTT	960
CTCTCTTCCT	ATCAATCCAT	CTTATTTGGA	AATGACTGTG	AGCGGACGAA	GCATCTGGAC	1020
CTGGTCATGC	TGGTGACAGA	GGTGATCGCC	TACTCCCACT	GCTGCATGAA	CCCGGTGATC	1080
TACGCCTTTG	TTGGAGAGAG	GTTCCGGAAG	TACCTGCGCC	ACTTCTTCCA	CAGGCACTTG	1140
CTCATGCACC	TGGGCAGATA	CATCCCATTc	CTTCCTAGTG	AGAAGCTGGA	AAGAACCAGC	1200
TCTGTCTCTC	CATCCACAGC	AGAGCCGGAA	CTCTCTATTG	TGTTTTAGGT	AGATGCAGAA	1260
AATTGCCTAA	AGAGGAAGGA	CCAAGGAGAT	NAAGCAAACA	CATTAAGCCT	TCCCACTCA	1320
CCTCTAAAC	AGTCCTTCAA	ACCTTCCAGT	GCAACACTGA	AGCTCTTAAG	ACACTGAAAT	1380
ATACACACAG	CAGTAGCAGT	AGATGCATGT	ACCCTAAGGT	CATTACCACA	GGCCAGGGCT	1440
GGGCAGCGTA	CTCATCATCA	ACCTAAAAAG	CAGAGCTTTG	CTTCTCTCTC	TAAAATGAGT	1500
TACCTATATT	TTAATGCACC	TGAATGTTAG	ATAGTTACTA	TATGCCGCTA	CAAAAAGGTA	1560
AAACTTTTTTA	TATTTTATAC	ATTAACCTCA	GCCAGCTATT	ATATAAATAA	AACATTTTCA	1620
CACAATACAA	TAAGTTAACT	ATTTTATTTT	CTAATGTGCC	TAGTTCTTTC	CCTGCTTAAT	1680
GAAAAGCTT						1689

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Thr	Ser	Leu	Asp	Thr	Val	Glu	Thr	Phe	Gly	Thr	Thr	Ser	Tyr	1	5	10	15
Tyr	Asp	Asp	Val	Gly	Leu	Leu	Cys	Glu	Lys	Ala	Asp	Thr	Arg	Ala	Leu	20	25	30	
Met	Ala	Gln	Phe	Val	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Thr	Phe	Gly	35	40	45	
Leu	Leu	Gly	Asn	Val	Val	Val	Val	Met	Ile	Leu	Ile	Lys	Tyr	Arg	Arg	50	55	60	
Leu	Arg	Ile	Met	Thr	Asn	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	65	70	75	80
Leu	Leu	Phe	Leu	Val	Thr	Leu	Pro	Phe	Trp	Ile	His	Tyr	Val	Arg	Gly	85	90	95	
His	Asn	Trp	Val	Phe	Gly	His	Gly	Met	Cys	Lys	Leu	Leu	Ser	Gly	Phe	100	105	110	
Tyr	His	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	115	120	125	
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	130	135	140	
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Val	Thr	Trp	Gly	Leu	145	150	155	160
Ala	Val	Leu	Ala	Ala	Leu	Pro	Glu	Phe	Ile	Phe	Tyr	Glu	Thr	Glu	Glu	165	170	175	
Leu	Phe	Glu	Glu	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Pro	Glu	Asp	Thr	Val	180	185	190	
Tyr	Ser	Trp	Arg	His	Phe	His	Thr	Leu	Arg	Met	Thr	Ile	Phe	Cys	Leu	195	200	205	
Val	Leu	Pro	Leu	Leu	Val	Met	Ala	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	210	215	220	
Thr	Leu	Leu	Arg	Cys	Pro	Ser	Lys	Lys	Lys	Tyr	Lys	Ala	Ile	Arg	Leu	225	230	235	240
Ile	Phe	Val	Ile	Met	Ala	Val	Phe	Phe	Ile	Phe	Trp	Thr	Pro	Tyr	Asn	245	250	255	

CCCTTGGGCGG

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
260 265 270
Cys Glu Arg Thr Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285
Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300
Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320
Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
325 330 335
Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
340 345 350
Ile Val Phe
355

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1193 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 92..1156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTGTGCTTAT CCGGGCAAGA ACTTATCGAA ATACAATAGA AGACCCACGC GTCCGGTTTT	60
TACTTAGAAG AGATTTTCAG GGAGAAGTGA A ATG ACA ACC TCA CTA GAT ACA	112
Met Thr Thr Ser Leu Asp Thr	
1 5	
GTT GAG ACC TTT GGT ACC ACA TCC TAC TAT GAT GAC GTG GGC CTG CTC	160
Val Glu Thr Phe Gly Thr Thr Ser Tyr Tyr Asp Asp Val Gly Leu Leu	
10 15 20	
TGT GAA AAA GCT GAT ACC AGA GCA CTG ATG GCC CAG TTT GTG CCC CCG	208
Cys Glu Lys Ala Asp Thr Arg Ala Leu Met Ala Gln Phe Val Pro Pro	
25 30 35	
CTG TAC TCC CTG GTG TTC ACT GTG GGC CTC TTG GGC AAT GTG GTG GTG	256
Leu Tyr Ser Leu Val Phe Thr Val Gly Leu Leu Gly Asn Val Val Val	
40 45 50 55	
GTG ATG ATC CTC ATA AAA TAC AGG AGG CTC CGA ATT ATG ACC AAC ATC	304
Val Met Ile Leu Ile Lys Tyr Arg Arg Leu Arg Ile Met Thr Asn Ile	
60 65 70	

CCGCGGTTTT

TAC	CTG	CTC	AAC	CTG	GCC	ATT	TCG	GAC	CTG	CTC	TTC	CTC	GTC	ACC	CTT	352
Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Leu	Val	Thr	Leu	
			75					80					85			
CCA	TTC	TGG	ATC	CAC	TAT	GTC	AGG	GGG	CAT	AAC	TGG	GTT	TTT	GGC	CAT	400
Pro	Phe	Trp	Ile	His	Tyr	Val	Arg	Gly	His	Asn	Trp	Val	Phe	Gly	His	
		90					95					100				
GGC	ATG	TGT	AAG	CTC	CTC	TCA	GGG	TTT	TAT	CAC	ACA	GGC	TTG	TAC	AGC	448
Gly	Met	Cys	Lys	Leu	Leu	Ser	Gly	Phe	Tyr	His	Thr	Gly	Leu	Tyr	Ser	
	105					110					115					
GAG	ATC	TTT	TTC	ATA	ATC	CTG	CTG	ACA	ATC	GAC	AGG	TAC	CTG	GCC	ATT	496
Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	
	120				125					130					135	
GTC	CAT	GCT	GTG	TTT	GCC	CTT	CGA	GCC	CGG	ACT	GTC	ACT	TTT	GGT	GTC	544
Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	Arg	Thr	Val	Thr	Phe	Gly	Val	
				140					145					150		
ATC	ACC	AGC	ATC	GTC	ACC	TGG	GGC	CTG	GCA	GTG	CTA	GCA	GCT	CTT	CCT	592
Ile	Thr	Ser	Ile	Val	Thr	Trp	Gly	Leu	Ala	Val	Leu	Ala	Ala	Leu	Pro	
			155					160					165			
GAA	TTT	ATC	TTC	TAT	GAG	ACT	GAA	GAG	TTG	TTT	GAA	GAG	ACT	CTT	TGC	640
Glu	Phe	Ile	Phe	Tyr	Glu	Thr	Glu	Glu	Leu	Phe	Glu	Glu	Thr	Leu	Cys	
		170					175					180				
AGT	GCT	CTT	TAC	CCA	GAG	GAT	ACA	GTA	TAT	AGC	TGG	AGG	CAT	TTC	CAC	688
Ser	Ala	Leu	Tyr	Pro	Glu	Asp	Thr	Val	Tyr	Ser	Trp	Arg	His	Phe	His	
	185					190					195					
ACT	CTG	AGA	ATG	ACC	ATC	TTC	TGT	CTC	GTT	CTC	CCT	CTG	CTC	GTT	ATG	736
Thr	Leu	Arg	Met	Thr	Ile	Phe	Cys	Leu	Val	Leu	Pro	Leu	Leu	Val	Met	
	200				205					210					215	
GCC	ATC	TGC	TAC	ACA	GGA	ATC	ATC	AAA	ACG	CTG	CTG	AGG	TGC	CCC	AGT	784
Ala	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	Thr	Leu	Leu	Arg	Cys	Pro	Ser	
				220					225					230		
AAA	AAA	AAG	TAC	AAG	GCC	ATC	CGG	CTC	ATT	TTT	GTC	ATC	ATG	GCG	GTG	832
Lys	Lys	Lys	Tyr	Lys	Ala	Ile	Arg	Leu	Ile	Phe	Val	Ile	Met	Ala	Val	
			235					240					245			
TTT	TTC	ATT	TTC	TGG	ACA	CCC	TAC	AAT	GTG	GCT	ATC	CTT	CTC	TCT	TCC	880
Phe	Phe	Ile	Phe	Trp	Thr	Pro	Tyr	Asn	Val	Ala	Ile	Leu	Leu	Ser	Ser	
		250					255					260				
TAT	CAA	TCC	ATC	TTA	TTT	GGA	AAT	GAC	TGT	GAG	CGG	AGC	AAG	CAT	CTG	928
Tyr	Gln	Ser	Ile	Leu	Phe	Gly	Asn	Asp	Cys	Glu	Arg	Ser	Lys	His	Leu	
	265					270					275					
GAC	CTG	GTC	ATG	CTG	GTG	ACA	GAG	GTG	ATC	GCC	TAC	TCC	CAC	TGC	TGC	976
Asp	Leu	Val	Met	Leu	Val	Thr	Glu	Val	Ile	Ala	Tyr	Ser	His	Cys	Cys	
	280				285					290					295	
ATG	AAC	CCG	GTG	ATC	TAC	GCC	TTT	GTT	GGA	GAG	AGG	TTC	CGG	AAG	TAC	1024
Met	Asn	Pro	Val	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Arg	Phe	Arg	Lys	Tyr	
				300					305						310	

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CTG CGC CAC TTC TTC CAC AGG CAC TTG CTC ATG CAC CTG GGC AGA TAC	1072
Leu Arg His Phe Phe His Arg His Leu Leu Met His Leu Gly Arg Tyr	
315 320 325	
ATC CCA TTC CTT CCT AGT GAG AAG CTG GAA AGA ACC AGC TCT GTC TCT	1120
Ile Pro Phe Leu Pro Ser Glu Lys Leu Glu Arg Thr Ser Ser Val Ser	
330 335 340	
CCA TCC ACA GCA GAG CCG GAA CTC TCT ATT GTG TTT TAGGTAGATG	1166
Pro Ser Thr Ala Glu Pro Glu Leu Ser Ile Val Phe	
345 350 355	
CAGAAAATTG CCTAAAGAGG AAGGACC	1193

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr	
1 5 10 15	
Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu	
20 25 30	
Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly	
35 40 45	
Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg	
50 55 60	
Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp	
65 70 75 80	
Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly	
85 90 95	
His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe	
100 105 110	
Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr	
115 120 125	
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala	
130 135 140	
Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu	
145 150 155 160	
Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu	
165 170 175	
Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val	
180 185 190	

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Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
195 200 205

Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220

Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240

Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
245 250 255

Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
260 265 270

Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
275 280 285

Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300

Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305 310 315 320

Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
325 330 335

Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
340 345 350

Ile Val Phe
355

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGGGAGAAG TGAAATGACA ACCTCACTAG ATACAGTTGA GACCTTTGGT ACCACATCCT	60
ACTATGATGA CGTGGGCCCTG CTCTGTGAAA AAGCTGATAC CAGAGCACTG ATGGCCCACT	120
TTGTGCCCCC GCTGTACTCC CTGGTGTTC A CTGTGGGCCT CTTGGGCAAT GTGGTGGTGG	180
TGATGATCCT CATAAAATAC AGGAGGCTCC GAATTATGAC CAACATCTAC CTGCTCAACC	240
TGGCCATTTC GGACCTGCTC TTCCTCGTCA CCCTTCCATT CTGGATCCAC TATGTCAGGG	300
GGCATAACTG GGTTTTTTGGC CATGGCATGT GTAAGCTCCT CTCAGGGTTT TATCACACAG	360
GCTTGATACAG CGAGATCTTT TTCATAATCC TGCTGACAAT CGACAGGTAC CTGGCCATTG	420
TCCATGCTGT GTTTGCCCTT CGAGCCCGGA CTGTCACTTT TGGTGTCATC ACCAGCATCG	480
TCACCTGGGG CCTGGCAGTG CTAGCAGCTC TTCCTGAATT TATCTTCTAT GAGACTGAAG	540

(2) INFORMATION FOR SEQ ID NO:6:

(A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met 1	Thr	Thr	Ser	Leu 5	Asp	Thr	Val	Glu	Thr 10	Phe	Gly	Thr	Thr	Ser 15	Tyr
Tyr	Asp	Asp	Val 20	Gly	Leu	Leu	Cys	Glu 25	Lys	Ala	Asp	Thr	Arg 30	Ala	Leu
Met	Ala	Gln 35	Phe	Val	Pro	Pro	Leu 40	Tyr	Ser	Leu	Val	Phe 45	Thr	Val	Gly
Leu	Leu 50	Gly	Asn	Val	Val	Val 55	Val	Met	Ile	Leu	Ile 60	Lys	Tyr	Arg	Arg
Leu 65	Arg	Ile	Met	Thr	Asn 70	Ile	Tyr	Leu	Leu	Asn 75	Leu	Ala	Ile	Ser	Asp 80
Leu	Leu	Phe	Leu	Val 85	Thr	Leu	Pro	Phe 90	Trp	Ile	His	Tyr	Val	Arg 95	Gly
His	Asn	Trp	Val 100	Phe	Gly	His	Gly	Met 105	Cys	Lys	Leu	Leu	Ser 110	Gly	Phe
Tyr	His	Thr 115	Gly	Leu	Tyr	Ser	Glu 120	Ile	Phe	Phe	Ile	Ile 125	Leu	Leu	Thr
Ile	Asp 130	Arg	Tyr	Leu	Ala	Ile 135	Val	His	Ala	Val	Phe 140	Ala	Leu	Arg	Ala
Arg 145	Thr	Val	Thr	Phe	Gly 150	Val	Ile	Thr	Ser	Ile 155	Val	Thr	Trp	Gly	Leu 160

-139-

Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
165 170 175
Leu Phe Glu Glu Thr Xaa Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
180 185 190
Tyr Ser Trp Xaa Xaa Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
195 200 205
Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
210 215 220
Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
225 230 235 240
Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
245 250 255
Val Ala Ile Leu Leu Ser Xaa Xaa Xaa Xaa Ile Leu Phe Gly Asn Asp
260 265 270
Cys Glu Arg Xaa Xaa Xaa Xaa Asp Leu Val Met Leu Val Thr Glu Val
275 280 285
Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
290 295 300
Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Xaa Phe His Arg His Leu
305 310 315 320
Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
325 330 335
Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
340 345 350
Ile Val Phe
355

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TACCTGCTSA ACCTGGCCNT GGCNG

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /mod_base= i

- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCTGGCCNT GGCNGACCTM CTCTT

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACCGYTACC TGGCCATNGT CCAYGCC

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGCRTGGACN ATGGCCAGGT ARCGGTC

27

460077 55555555

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

NACCANRTTG TAGGGNRNCC ARMARAG

27

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGTAGGGNRN CCARMARAGR AGNARGAA

28

46607 333630

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 12
(D) OTHER INFORMATION: /mod_base= i

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 15
(D) OTHER INFORMATION: /mod_base= i

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 16
(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAGGCGTAG ANSANNGGGT TGASGCA

27

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 4
(D) OTHER INFORMATION: /mod_base= i

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 7
(D) OTHER INFORMATION: /mod_base= i

- (ix) FEATURE:
(A) NAME/KEY: modified_base
(B) LOCATION: 8
(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGANSANNGG GTTGASGCAG CWGTG

25

CCCTGGGCG

18